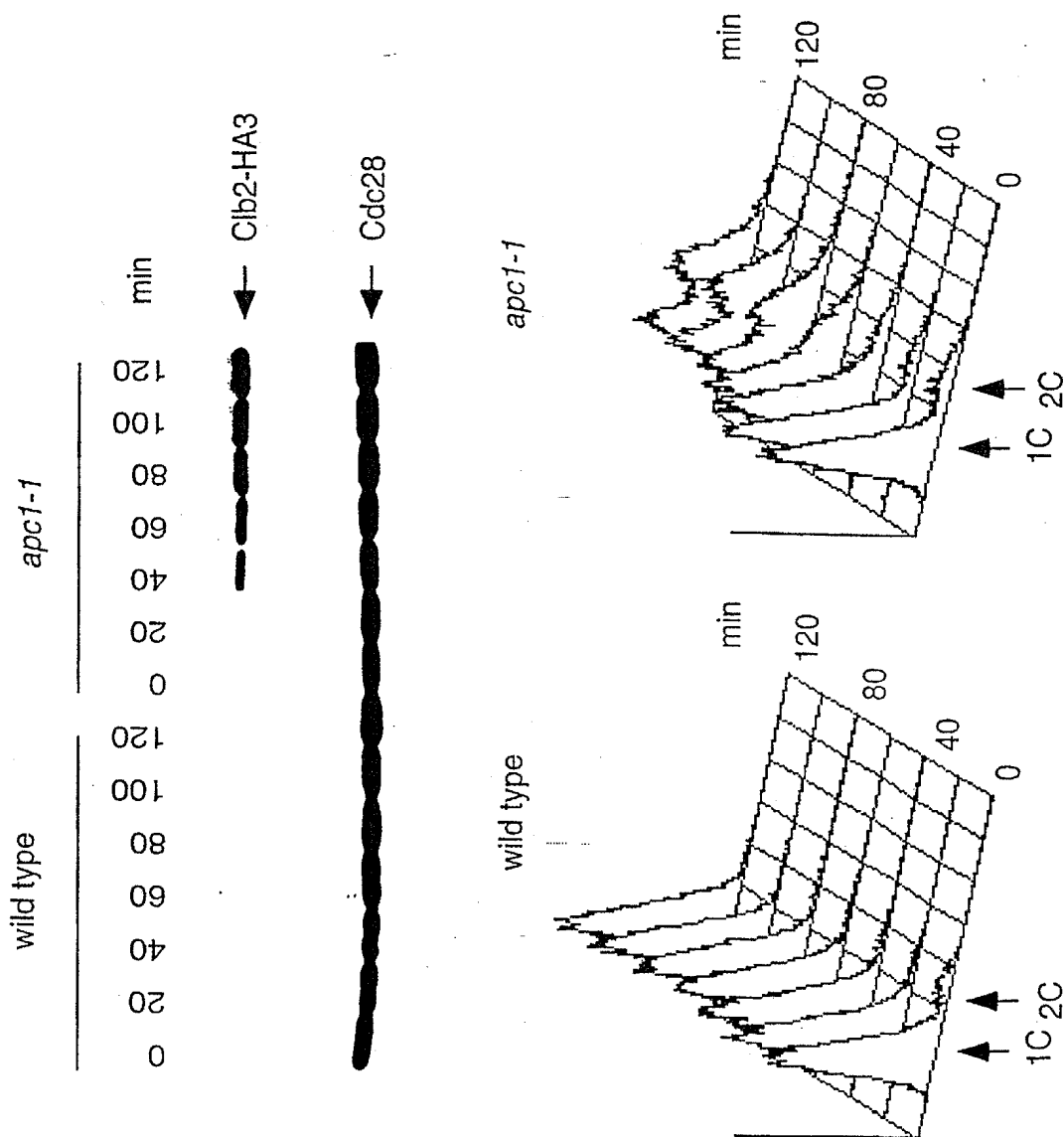
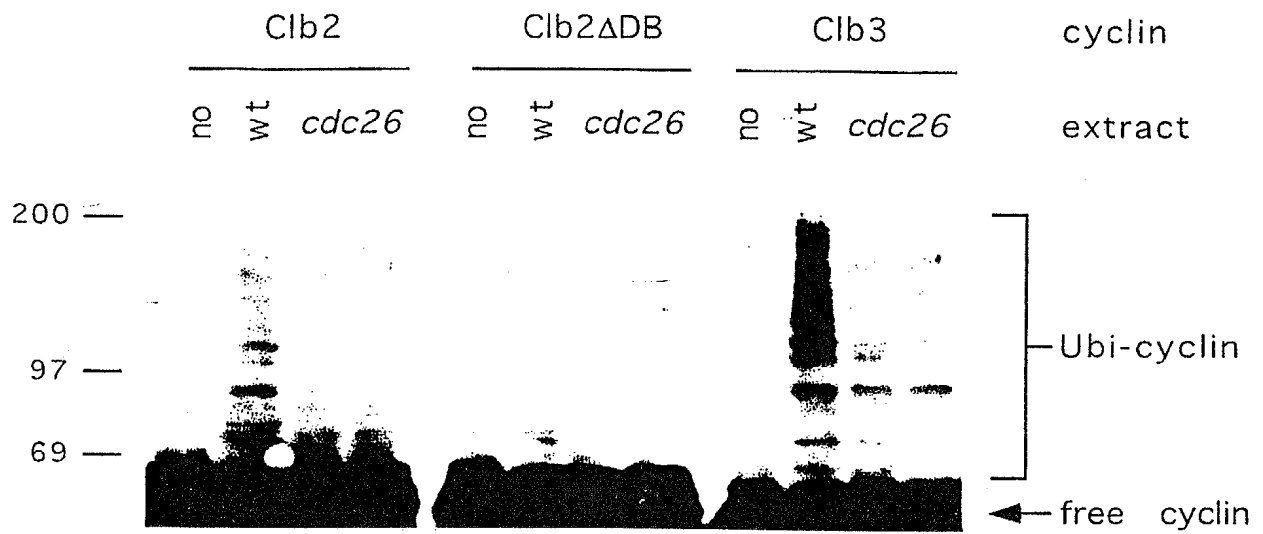


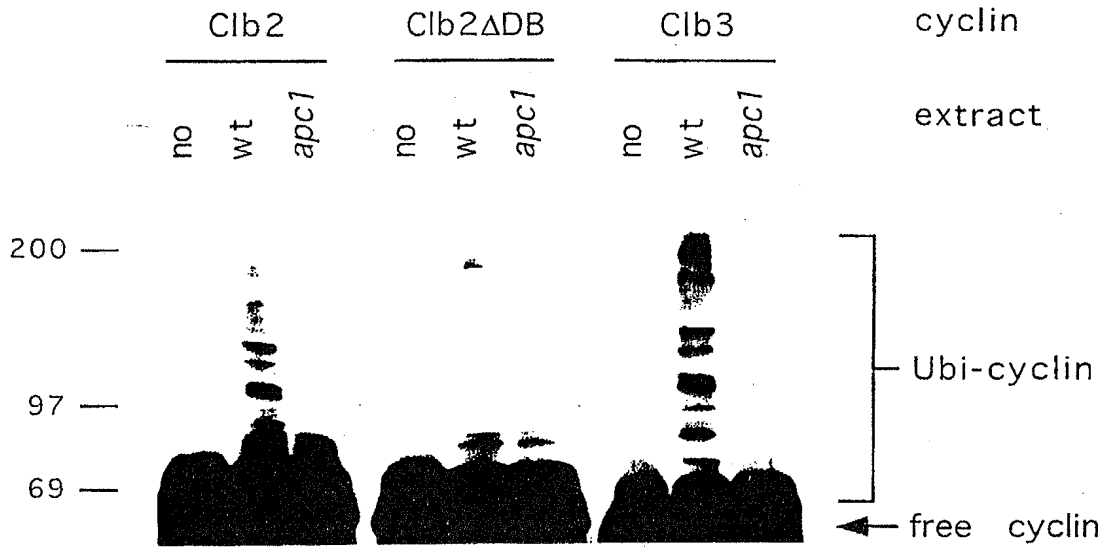
1/22
Fig. 1A

APPROVED	DATE	BY	CLASS
0.6.FIG.			
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662030-60190260

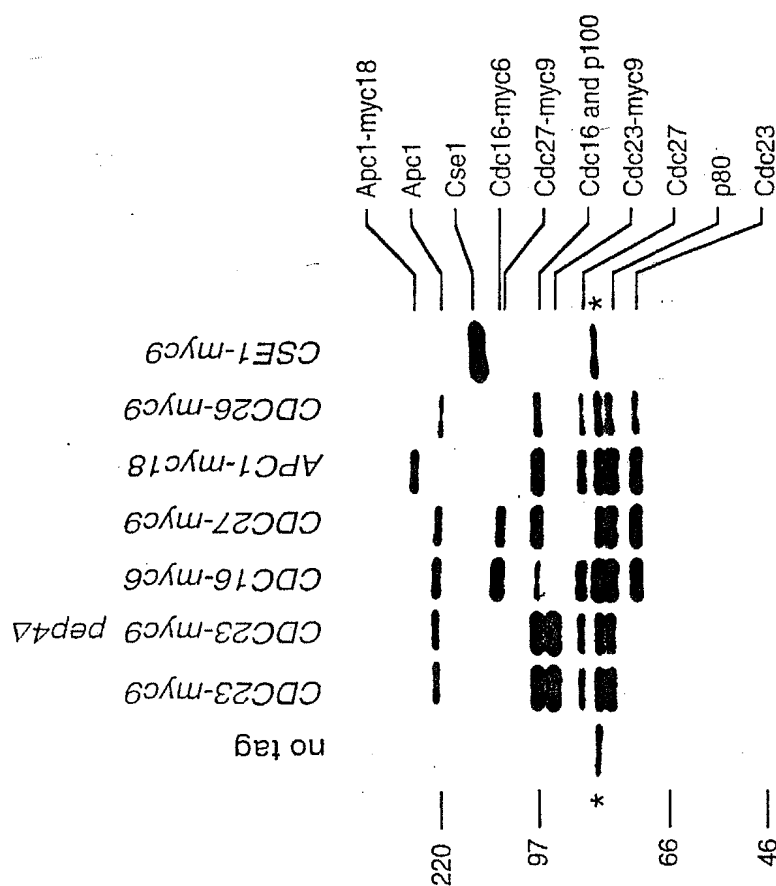


2/22
Fig.1B

3/22
Fig. 1C

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5/22
Fig. 2B



APPROVED BY CLASS COUNCIL CLASS CRAFTSMAN

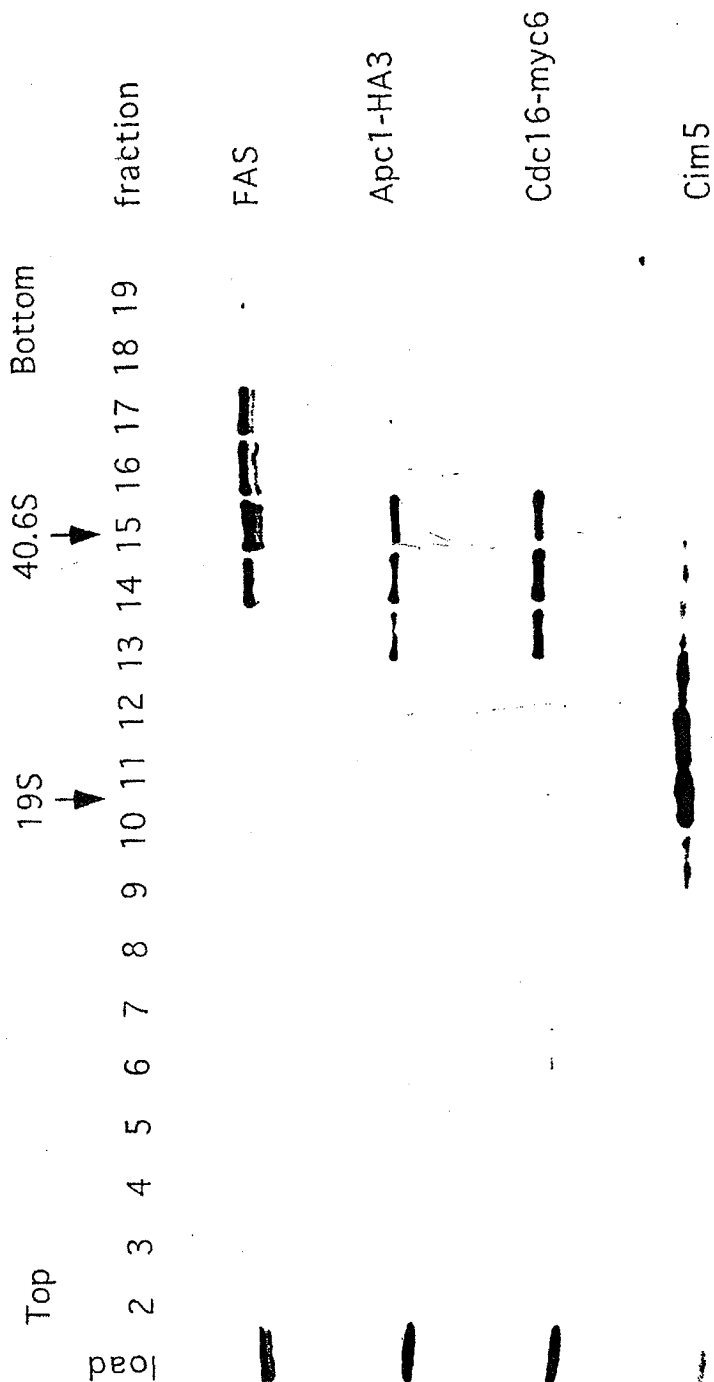
WO 98/21326

09/308109

PCT/EP97/06268

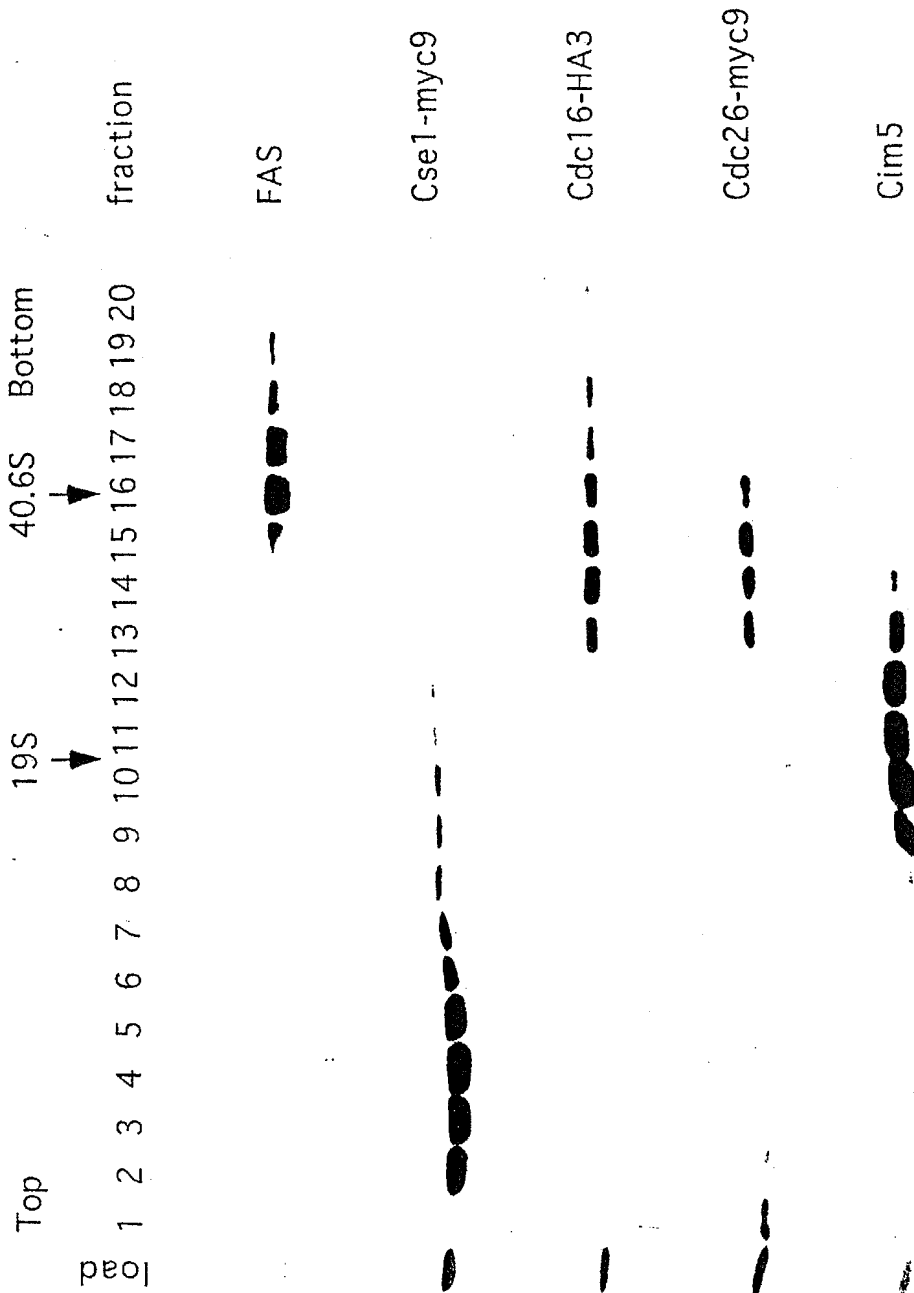
6/22
Fig. 3A

APPROVED	0.6 FIG.
BY	CLASS
DATE	



7/22
Fig. 3B

APPROVED	0.6.FIG.
BY	DATE
EMITTED	RECEIVED

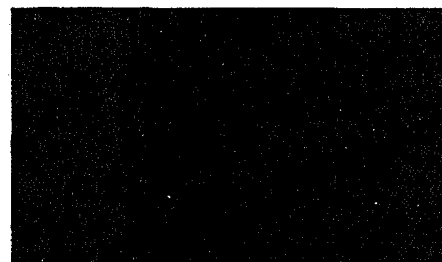
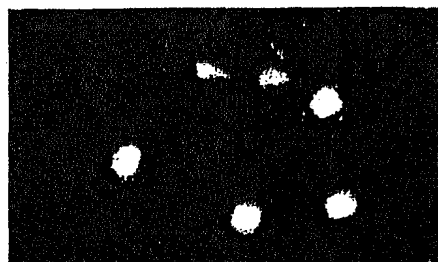
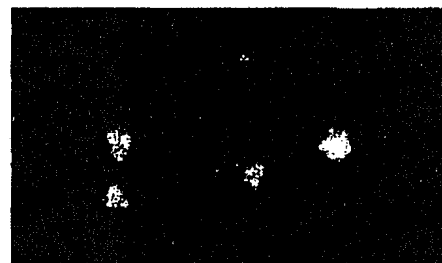
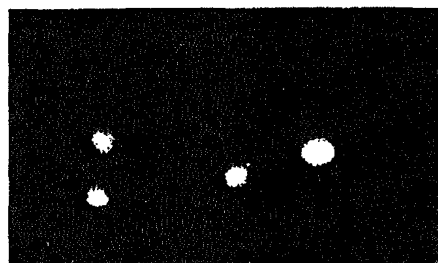
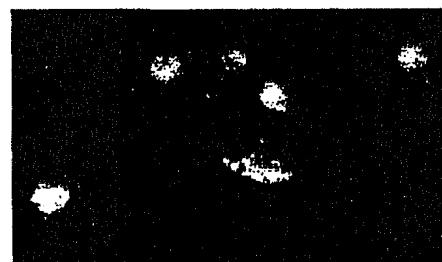
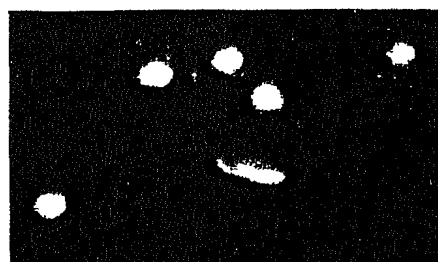


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Fig. 4

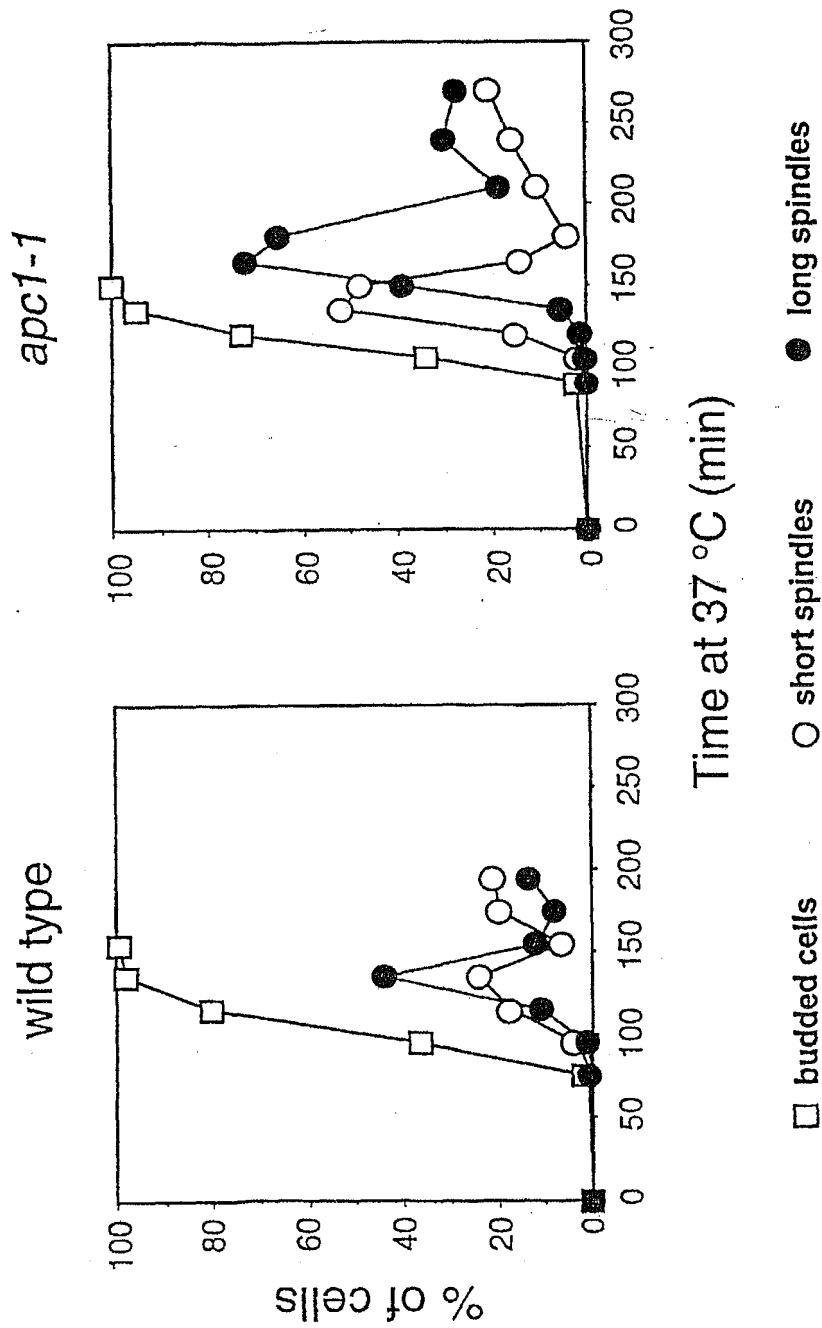
DAPI

anti-myc

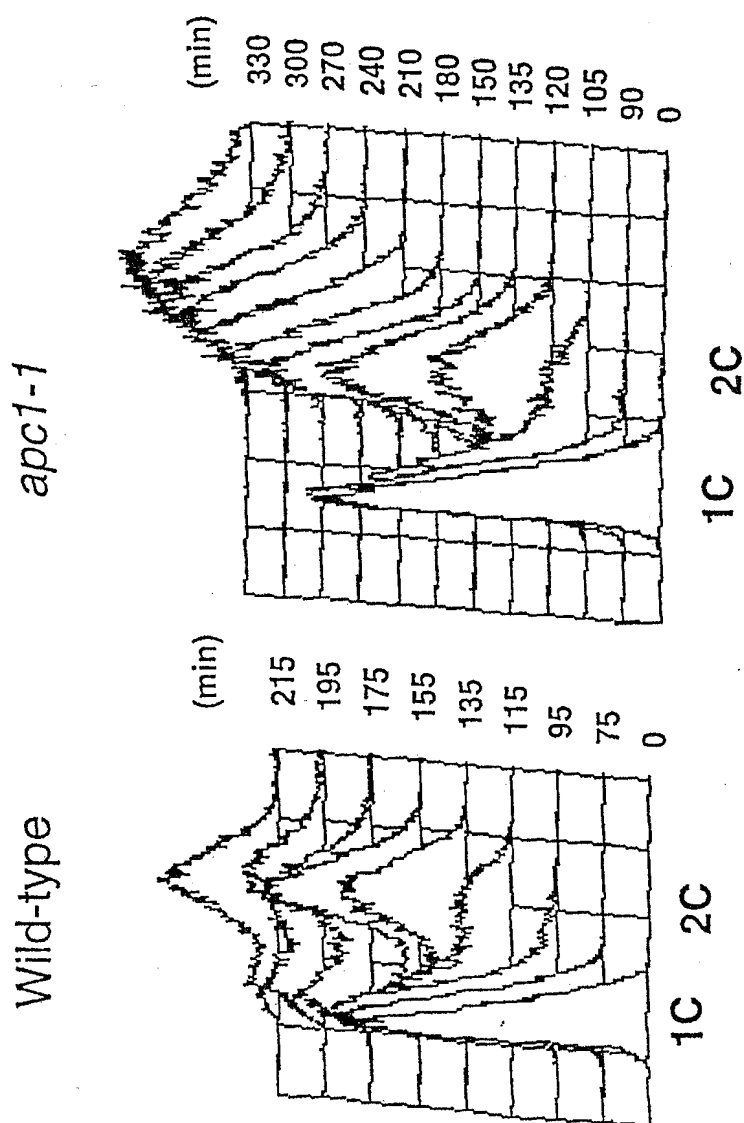
no myc

*CDC16-
myc6**CDC26-
myc9**APC1-
myc18*

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Fig. 5A

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Fig. 5B

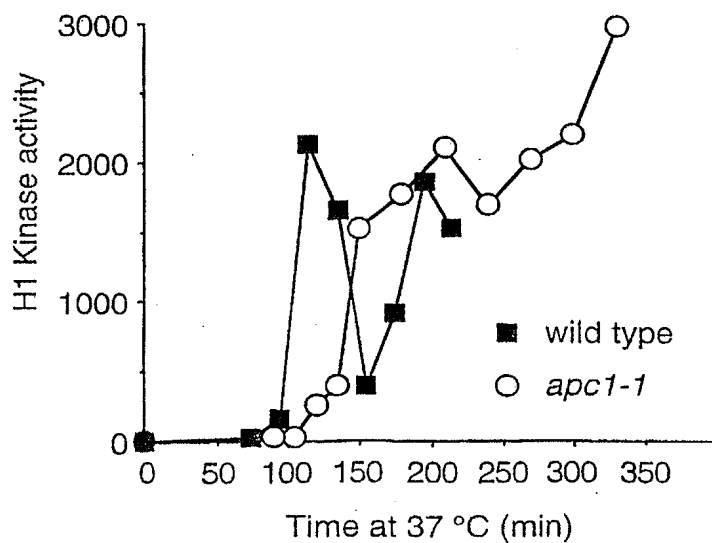
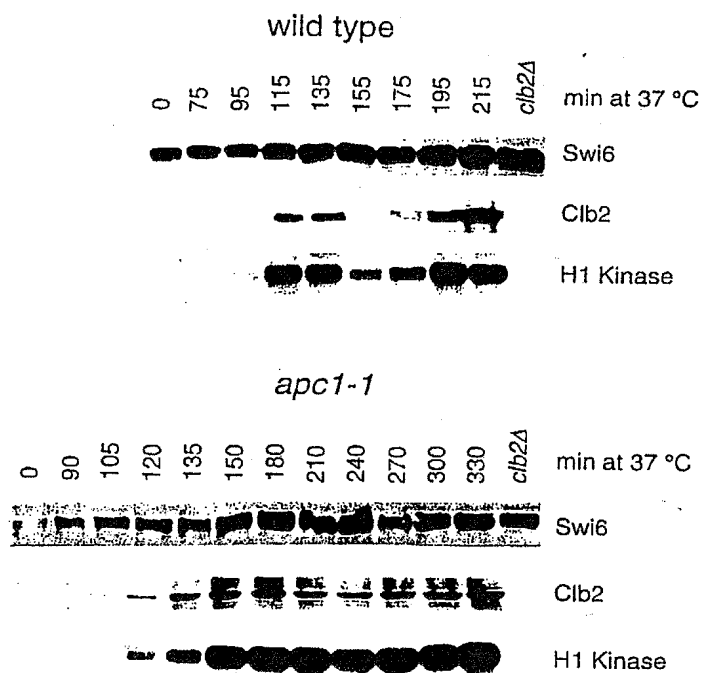


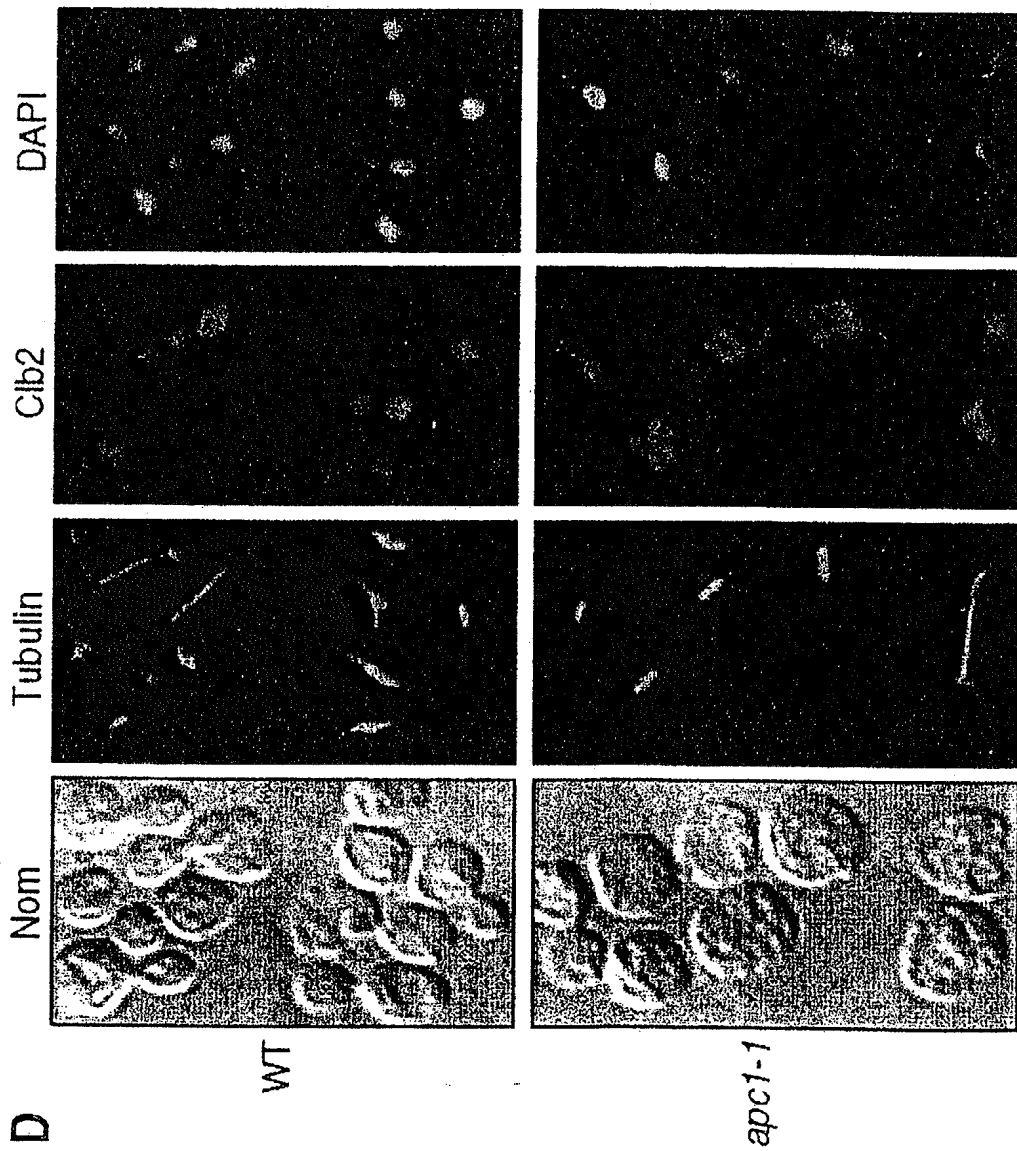
APC1-1
BY
DRAFTING
D.C. FIG.
CLASS. DESCLASO

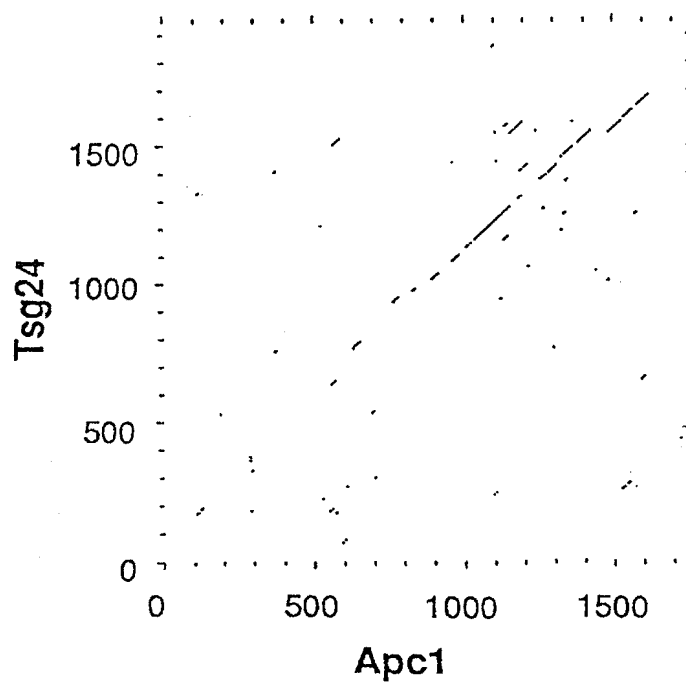
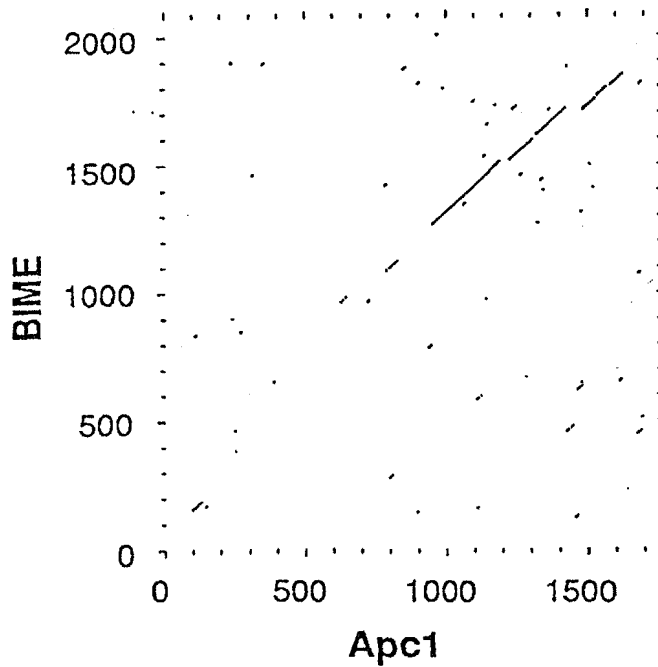
662099-60130660

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Fig. 5C



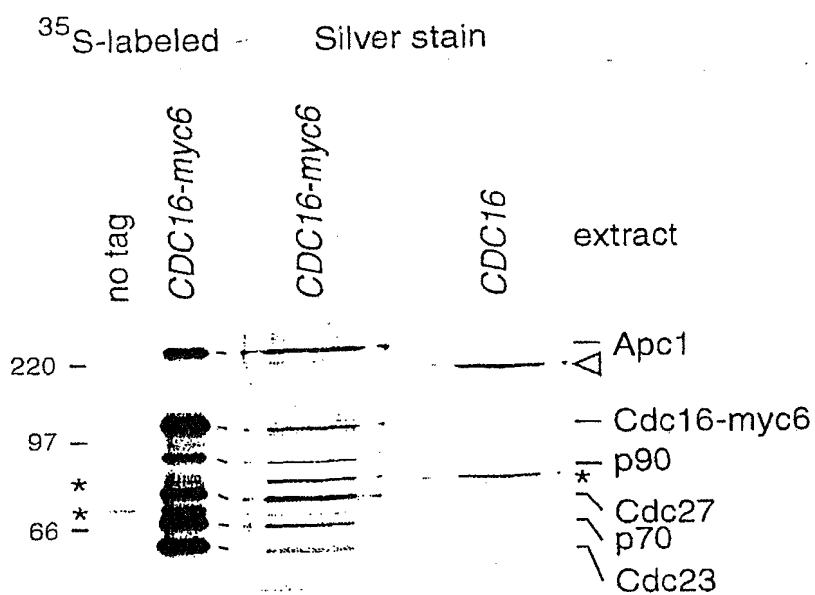
12/22
Fig. 5D

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Fig. 6A

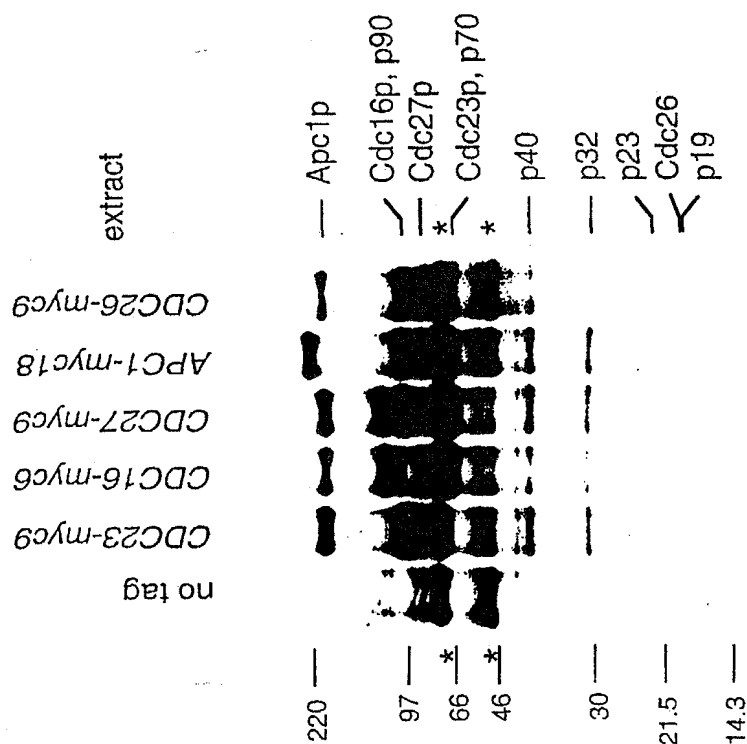
14/22
Fig. 6B

apc1	AGCTGSGEGRKFTHEVSTAYVYRTRTKQFFT.TKTEYAQIITACILYFAKIMALECTNCGVG	960
bime	..LTFREDKREIEAARLTNQSKAPAAECHVPEBWTOSDLLEAQLQEVVOLVTLTSLITG	1274
tsg24	..LHWSEDLRVQHVRRLQSAQEVVRVNVQYDELSDEHFEITEENRRLQLCQRTHALPVG	1083
Consensus	--LTFSEDKRF-HV-RLT-----P-----PE--D-----LE-KT-----LRT-----PVG	1366
apc1	AGAVAYATEKPISTORNVTOPLNISVFE..DDKITVKKAPEIDAHDIVEWQGHAGVGS	1018
bime	RAMLAFSGRLPLLEKLPDPSFSLQCCHKKSNNVPTISADRASFH.EEKICUAFPHNGUST	1332
tsg24	GLKFTLFSYHVPVPEPEPEVEKLELTGGRAPERNTAVDLNDSGNIQVPPNMASSVASPHNGVAA	1143
Consensus	RGM-A-----P--TEKLPF-LNL--V-EE-N-N-----N--D-----VA-PHNGVS-	1426
apc1	GLRISKKATGTCSTVAENKRP..ELDAYHGGFLGLGLNCHLKNTEEVHLYNYLSRHT	1076
bime	GLAISAKKSGIDTSVLEKNEB..ELTWRRHACFLALGLNCHLRS.LAKMVAFKDYLRKHA	1390
tsg24	GLKTAASQ.LDSAWAVYRPHHAELANAYACFLMALGLNCHLTKLATLNLTHLAKGHE	1202
Consensus	GL-ISK-S-GID-SWI-FNEPY--EL-N-HAGFLALGLNCHL--LA-M-I--YITE-HT	1486
apc1	HISTGLLGLGMSSEMKKSGNDGLKLVSVHVLNATLPSGSSDLNIDLRKLOTAGIICMCHLYL	1136
bime	NTSAGLLGLGSAASKLGAMDGLVTRLLSVHVTMRPMGSAABELNLSPLTOTAGIICMCHLYL	1450
tsg24	NTSICGLLGSAASKLGAMDHSITRLLSIHVPLLEPPTSTELDVPHNVQAAAVVGGGVQ	1262
Consensus	NTSICGLLG-SAS-LGAMD--TRLLSVHV-A-LP-GS-ELN-----OTAGI-GIGLY-	1546
apc1	NSRHRRNSDSIFAQLVSLNVDHDMVAD..EYRLAAGISGLKALGACQTKLRKWD	1192
bime	NSQHRRNSDSVMSLSEENADQEEGSGATNDYLRNRSYRLAAGLALGMLGCHG.....K	1302
tsg24	GTAMHHTAEVLLAEGRPPFGPEMEYCTD..RNSYRLAAGLALGMLGCHG.....S	1311
Consensus	NS-HRRNSEV-LAEI-----E-E--D-----E-YRLAAG-ALG-ENLG-G-----S	1606
apc1	SLGLGGLD.DLPEDVYDSSDVEQNVMYEDLTCLKLEIVTSTY.DTFENDWTPENSQICAVTA	1250
bime	DLKGRGDDHMHIVERGLAVAGT..ENDDLAHVLDRTATGATTA	1542
tsg24	NLIGNSDLNVPEQLTYQMYGCHRRRFQTMHREKHKSPSYQIEGDTINZ.DVTCPCATTA	1370
Consensus	-L-GH-D--PE-LY--VG-----H--D--V-D-----CATTA	1666
apc1	IMFLELZSNNGFISNMKVDLKEIKKANENTRPELLMYREMASNMILVEFICGDDLSFIMK	1310
bime	LAIMHEKTNDETSLAQKVDIPDTTVRFDYV..RPELFLRLTLARHILMDRIQACDENFIG	1600
tsg24	LAIMHYKTNDRSTADWRAPDPMYLDYV..KPEFLLRLTLARCLRLWDILPNSKHVS	1428
Consensus	LA-IFLETNN--IA--L--PDT--L-D-V--RPEULLRLTLAR--ILWD-I-----H--	1726
apc1	DM.....DIGVKFSE..LNTDLLPIYTHAGRILANGIRFASTGNLKIENIL	1355
bime	SLBEVYR..RRYRITGVRLLKSDMPF..FNITAGLCHALGRFAGSPDPTVRDIL	1652
tsg24	NVPEQYIRNSISLSEHRLPCSEDLNLEWLSQAHVYTIAGACLSLGRFAGSENLSAFSL	1488
Consensus	-VE--R--L--N--SED--L-M-----YTIAG-CLALG-RFAGS-NIL--R-IL	1786
apc1	LSLVDKFLPLYQYFGKONLDFRUTISVINVLTNVTVVSLSHVMCASGDLEVLRRVYLYHE	1415
bime	LSYLDQFIRISRLSPAENYDARLARNSVRHKQDVVALSLAAVHAGTGDLALFERLRLSLH	1710
tsg24	HKFAKDEMYN..LSAENASVTGPYNLETCLSVVLSLAAVHAGSGHRLVQLCRFLH	1543
Consensus	LS--D-E-----LPA-EN-D-PL--G--VY-LSLAAVHAGSGDL-VLRR-R-DH-	1846
apc1	VASGPYSDLFQEIPISSKSDVSGVTQVTSNTNTPGNSDRERVDETAASLDDERSNGSDIS	1475
bime	1710
tsg24	1543
Consensus	-----	1906
apc1	DPTAYLEDKDKIDDHVYGFISTHLAGFLFLGSGQVANTSTMTESIAFLSMSVLTFTYTP	1535
bimeGRVDPTDFYGSMMHNAHMAIGMLFLGCGSVTLGTSNLAIVASLIC.SLYPIPTT	1762
tsg24MKTGEMNVYGFHLHMAHLAGLFLGCGGSVLTSTNSVSIALLC.ALYPHREAH	1595
Consensus	-----K-D-D--YG-H-A-HMALG-LFLGCG-Y-L-TSNL--ALLC-SLYP-PET-	1966
apc1	..HPLQELHFFUSINVEPRCLVIKDISTGDAVNNVPIELVVEEDVEKEEVIREISTP	1590
bime	VLONECHLQALRHLLVLAAPRCLVPRDLDSRRRI.SMPITVTDSDS....EGMSGTHTAP	1816
tsg24	STDMRYHLOALRHLLVLAAPRCLVPRDVDTNTHC.YALIEVAYKGTQWYEQTKESHMAP	1654
Consensus	--DM--HLOALRHLLVLAAPRCLVP-D-DT--C--PIEVT-----E-V--EL-AP	2026
apc1	CLLPDSKLYSIRVEMHCTEPDVNFTDYSA.SDFESGCTITVIOQRKE..SVFENKAS	1647
bime	CLLPDLNRHAKVEVLSPDVVEVLQEDDSNPGVREKHQCGDQSYILRRLEAT....YHETG	1871
tsg24	CLLPDLHLQMKMYRGERHVELIDLSHGEQHLRSTLSKDGVLVVKLEAGQLSYKEDDMG	1714
Consensus	CLLPDL--LY--V-E-E-VNEL--DF-N-----E-SGD--LY--REA--S--EEL-G	2086
apc1	FRNVEDIHVALKRRKAE..SKNYGRNLKNEQGNNTSSQLVESLGIQDLNVELDTLGS	1704
bime	S.GFFSSSLGLSAAQDILPSASTSGAQGKGLSPSALPNVSALSLKESHRTPEPAAQS	1930
tsg24	WQSLLAQTVARNSEARAFKPETISSFT....SDPALLSFAEYFCRPTVSMGPQEIHD	1769
Consensus	--S--TV-A--SAA--S--N-----S--AL--E-L-K--H-PK--LS	2146
apc1	AGNNTALT	1713
bime	IWDWTFQL	1939
tsg24	LFSSIL.YE1777	
Consensus	-----I--D2155	

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Fig. 7A



16/22
Fig. 7B

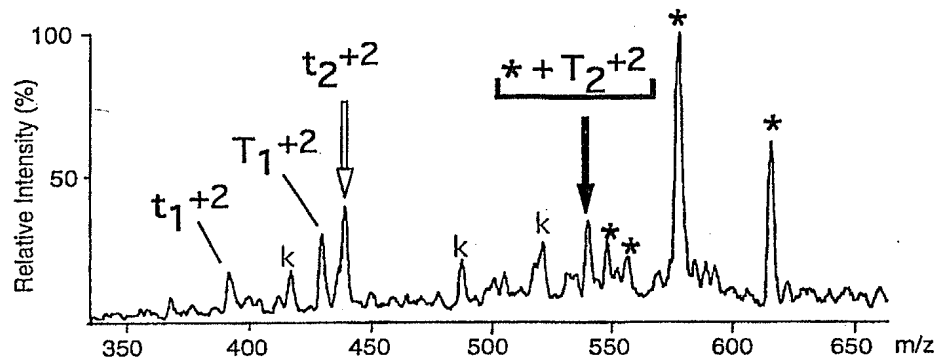


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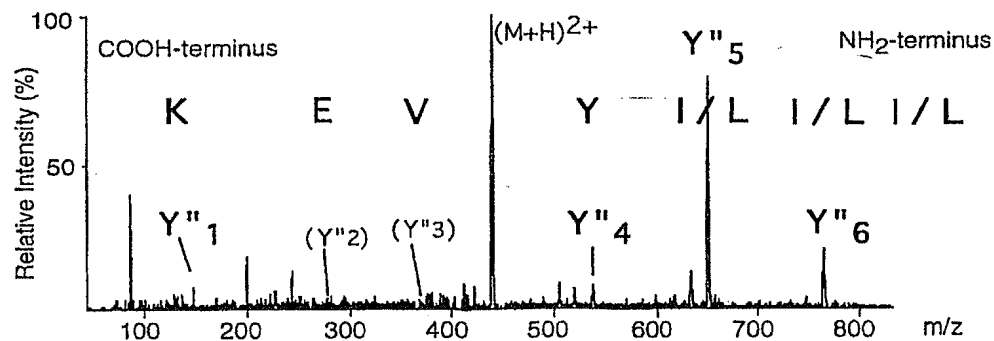
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Fig. 8

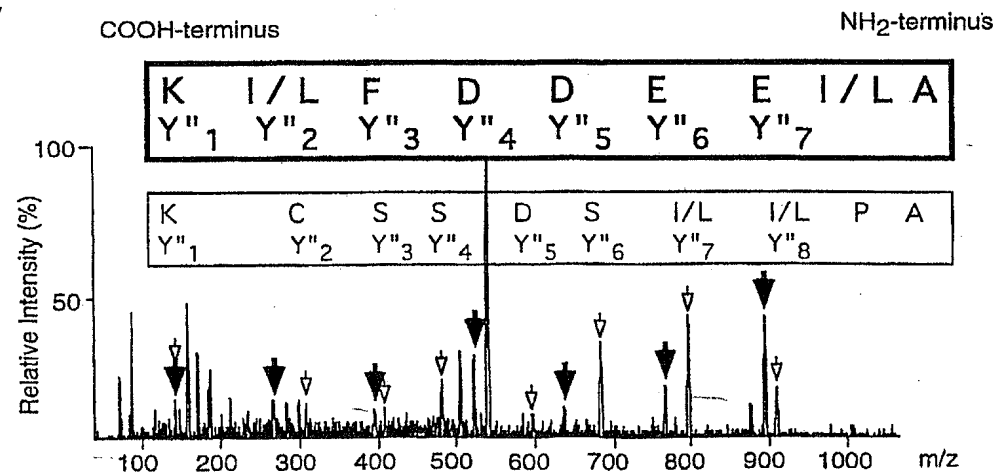
A



B

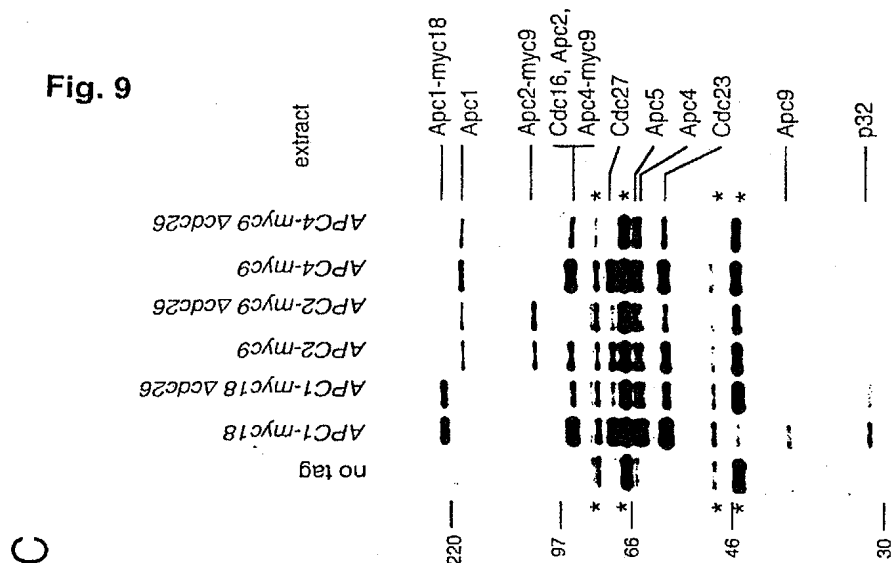


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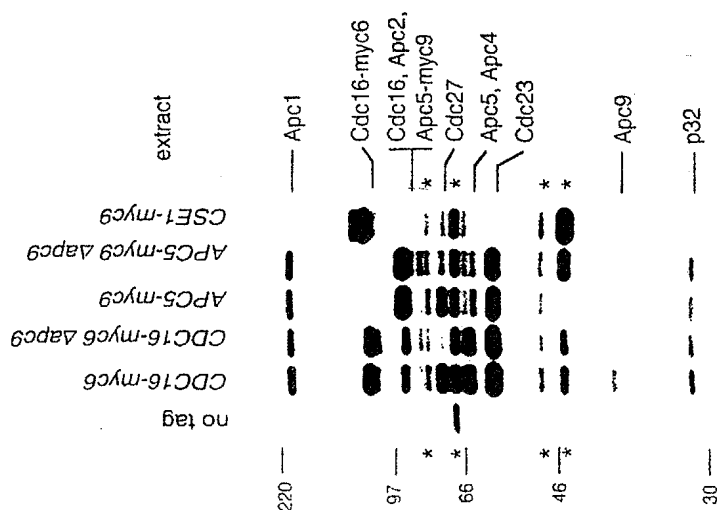
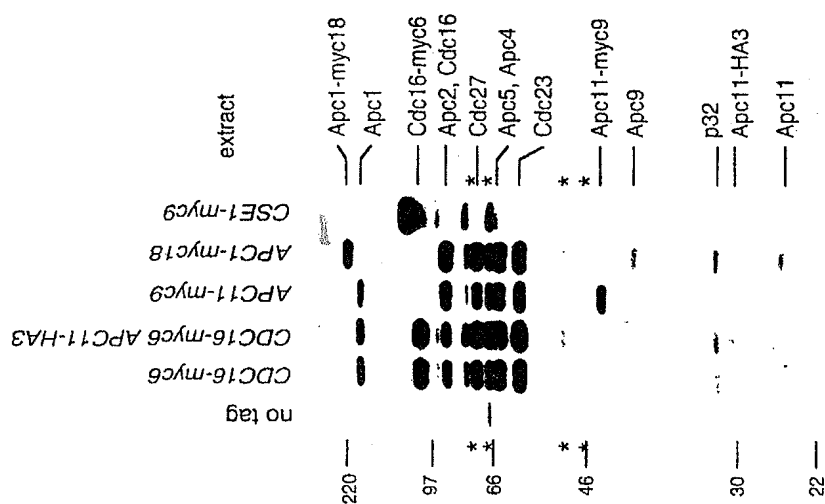


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Fig. 9



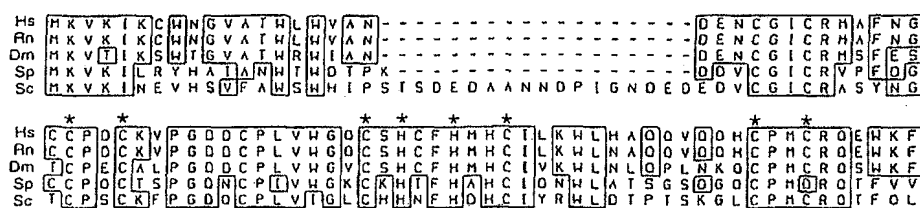
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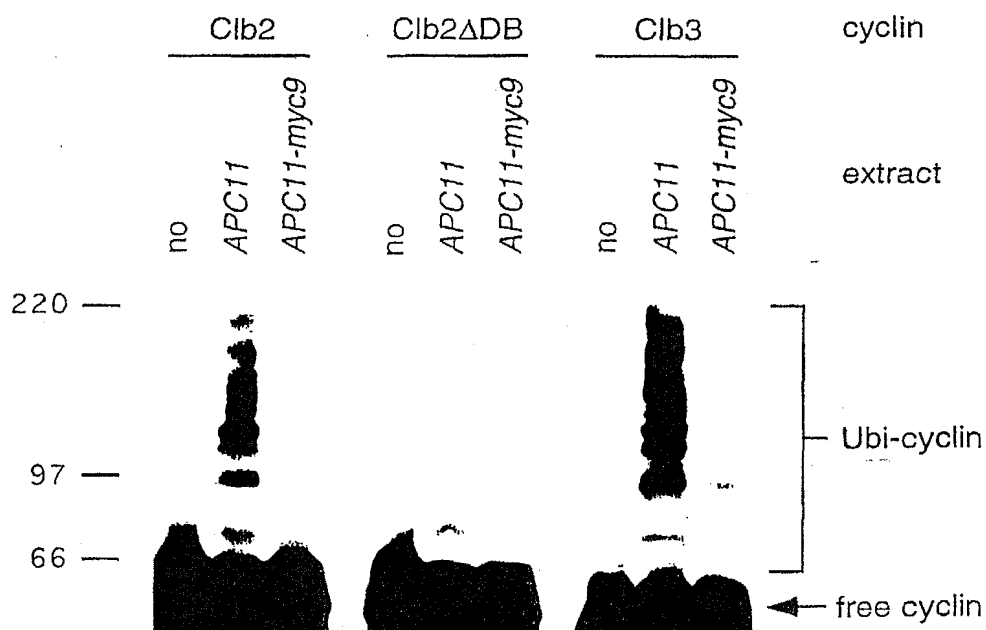
A

19/22
Fig. 10

A



B



20/22
Fig. 11A

A

CeCui3 L F R Y L Q E K D V F E K Y Y F K Q Y L A K R R L L T D K S C S D D V E K A L L A K L K I T
HsCui3 V L F R F M Q E K D V F E R A Y Y F K K R G H L A K R R L L F L N G R K S V S D D V E K M H I S K L K I T
CeCui4 V L F R F Y L R Q E K D V F E R A Y Y F K K R G H L A K R R L L F L N G R K S V S D D V E K M H I S K L K I T
HsCui4a V L F R F F I H G K D V F E A F Y Y K K R G D L A K R R L L V G N H T S S A S D O A E E K S H I S K L K H Q
DmCui1 V V F F K Y I E D K D V F O K F Y Y A R K M L A K R R L V H G N O N S S A S D O A E E A M I S K L K Q
HsCui1 V V F F K Y I E D K D V F O K F Y Y A R K M L A K R R L V H G N O N S S A S D O A E E A M I S K L K Q
HsCui2 T V F F K Y I D O K D V F O K F Y Y A R K M L A K R R L V H G N O N S S A S D O A E E A M I S K L K Q
ScCdc53 T I F K Y L T D K O A F E T H Y Y R R L F A K R R L I H G T S S T S A E D E E N T I O R L O A
CeKOH7.5 H L L V S V Y G S K E L F Y K E Y Y R N L L A D R R L S S S D N K O P E F E K J R Y V L D L L K L
MmApc2 H L L V S I Y G S K D L F I N E Y Y R N L L A D R R L L H O F S F S P E R E T R N V L D L L K L
ScApc2 V L L D L F E S R E F F I S E F R N L L T D R L F T L K F Y Y T L D E K H T R C L K L I R

CeCui3 E C G C O F T Q K L E N H F R - - - - - D K E L H - - - - - T
HsCui3 E C G C A F T Y K L E G H F R - - - - - D M H I S - - - - - N
CeCui4 E C G S A F T Y K L E G H F R - - - - - D M H I S - - - - - N
HsCui4a E C G A A F T S K L E G H F R - - - - - D M E L S - - - - - K
DmCui1 A C G F E Y T V K L O R H F O - - - - - D I G V S - - - - - K
HsCui1 A C G F E Y T S K L O R H F O - - - - - D I G V S - - - - - K
HsCui2 A C G F E Y T S K L H R H F O - - - - - D H S V S - - - - - A
ScCdc53 A N S H E Y T G K L T K H F O - - - - - D T R L S - - - - - K
CeKOH7.5 R F O Y S E L Q H C E V H L K - - - - - D V I H S - - - - - L
MmApc2 R F G E A P H F C E V H L K - - - - - D M A O S - - - - - R
ScApc2 E K I V K F T E T S H S N Y I T N G I L G L E T T A P A A D A O O S N L N S I D V H L

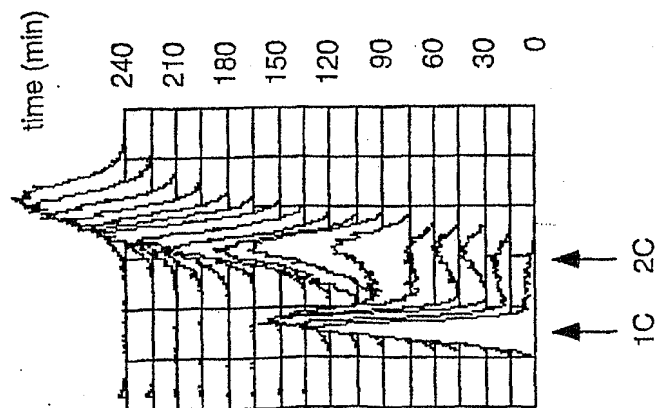
CeCui3 L A T S F R O W R E A Q P - T K M S - - I D I S L R V L T A G V H P T V O C N P - - - -
HsCui3 T H O E F R O W R L O A H M S - V S L G G - - V D L T V R V I T T G Y H P T V O S A T Y E - - - -
CeCui4 Y G R L F N Q Y L E A H M S - K E S G P - - N F L T V R V I T T G Y H P T Y T D T P M E - - - -
HsCui4a I H V F K Q Y L H O N O S - D S G P - - T D L T V N I L T H G Y H P T Y T D T P M E - - - -
DmCui1 L N S Y F K Q Y L A E K S N - E P L M E - - I D F G I O V L S S S G S W H P F F O O S N N T - - - -
HsCui1 L N E Q F K K K Y L T A E K S - E P L M E - - I D F G I O V L S S S G S W H P F F O O S N N T - - - -
HsCui2 L N N K F N N F I K N Q D P - T V S I D L G Y I S F O V L L A E A G A H P F L T S Y O A P S S T - - - -
ScCdc53 L E D F F A V A L K K N Q D P - T V S I D L G Y I S F O V L L A E A G A H P F L T S Y O A P S S T - - - -
CeKOH7.5 I D K K F F A V A L K K N Q D P - T V S I D L G Y I S F O V L L A E A G A H P F L T S Y O A P S S T - - - -
MmApc2 I N A N I R E E H S E R K R P - G N Y E Q V P P F G V A C V I L S S S E F H Y H P P F F L E T E K - - - -
ScApc2 H D T K C S E E L C R K H E V A G L O P T I F V P K F I S L S L L Y H K Y N C D T O G S N D

CeCui3 - - V V L P Q E L S V A F Y E I H F T R R O F Y Y T A K H T G R K L T I N O T L H G S N A D V K A T F F
HsCui3 - - C N I P P A P R H V A F Y E I H F T R R O F Y Y T A K H T G R K L T I N O T L H G S N A D V K A T F F
CeCui4 - - I N I P P A P R H V A F Y E I H F T R R O F Y Y T A K H T G R K L T I N O T L H G S N A D V K A T F F
HsCui4a - - V H L T P E M R I K L Q E V Y Y L R G V H G N R N K V L O H H G L A S A V I S K A E F F
DmCui1 - - F A L P S E L E R S V O R O F F N E A F Y Y A A R H S G R K L L N W H L Y O H C K G E L I H N V C
HsCui1 - - F A L P S E L E R S V O R O F F N E A F Y Y A A R H S G R K L L N W H L Y O H C K G E L I H N V C
HsCui2 - - F A L P S E L E R S V O R O F F N E A F Y Y A A R H S G R K L L N W H L Y O H C K G E L I H N V C
ScCdc53 - - F K L P K P L V P A H E X L K E E S Y L D V K H N D R K I L K H W L R S V G L C V E I V S I N I
CeKOH7.5 - - A L H P P L O A A A L D V Y C S K I Y L D V K H N D R K I L K H W L R S V G L C V E I V S I N I
MmApc2 - - L E V P I D I R A A L D V Y C S K I Y L D V K H N D R K I L K H W L R S V G L C V E I V S I N I
Apc2 L A F H L P I D L E R E L D Q V S C K I Y L D V K H N D R K I L K H W L R S V G L C V E I V S I N I

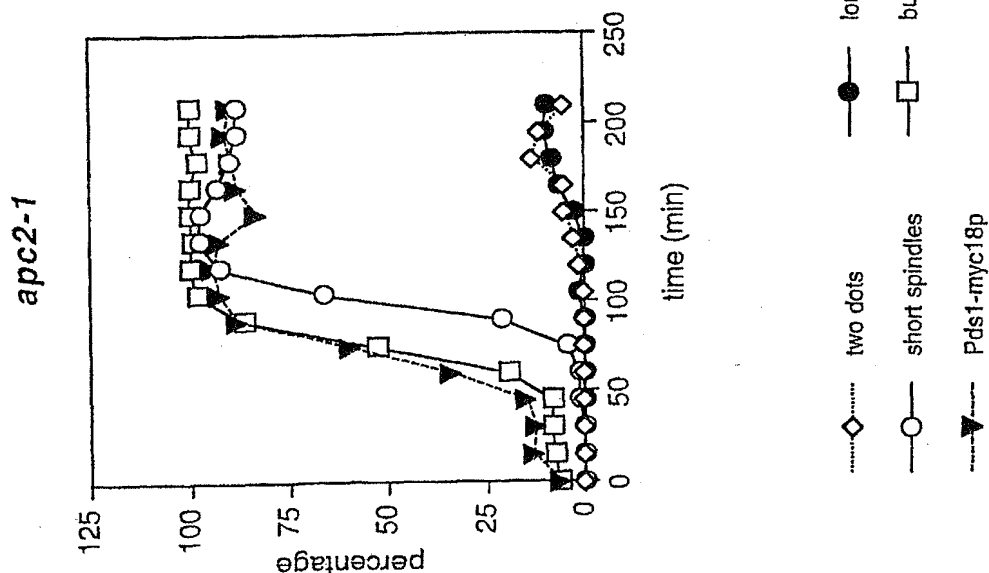
0.8. FIG.
CLASS (SUBCLASS)
BY
DRAFTSMAN

662090-60T00200

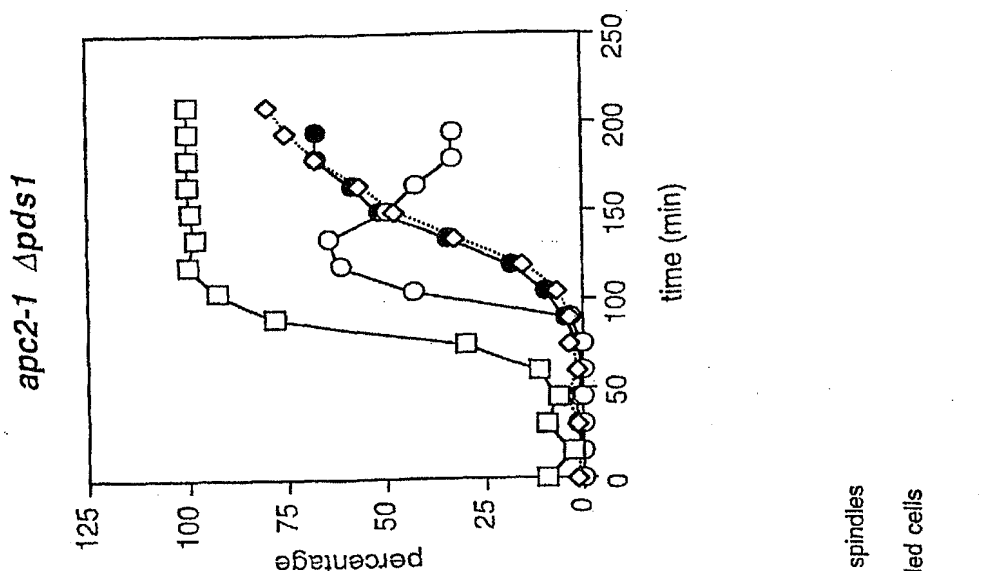
B



C



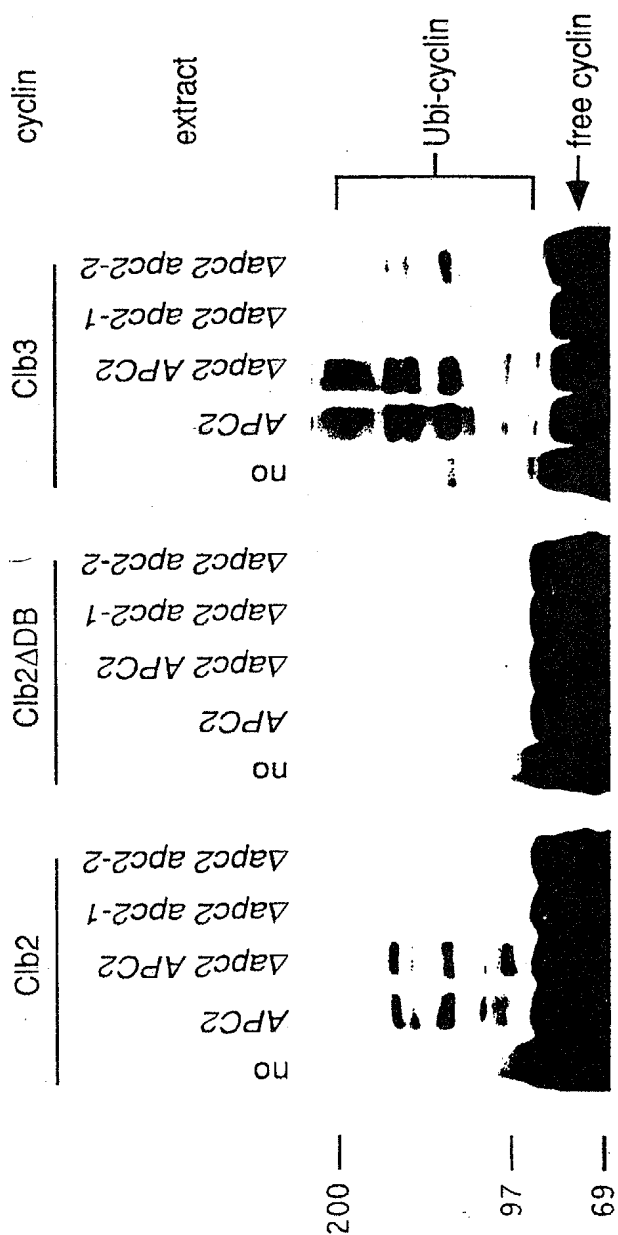
D



◇ two dots
 ○ short spindles
 ▼ Pds1-myc18p
 ● long spindles
 □ budded cells

Fig. 11B

22/22
Fig. 11C



660930-601202-00
APC2 0.4.FIG.
6/100 1000L83
DRAFTING